
CyVerse Documentation

Release 1.0

CyVerse

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CHAPTER 1

Goal

QIIME 2™ is a next-generation microbiome bioinformatics platform that is extensible, free, open source, and community developed.

- Automatically track your analyses with decentralized data provenance — no more guesswork on what commands were run!
- Interactively explore your data with beautiful visualizations that provide new perspectives.
- Easily share results with your team, even those members without QIIME 2 installed.
- Plugin-based system — your favorite microbiome methods all in one place.

In this quick start, we will show you how to launch JupyterLab-QIIME2 VICE app in DE

Prerequisites

2.1 Downloads, access, and services

In order to complete this tutorial you will need access to the following services/software

Prerequisite	Preparation/Notes	Link/Download
CyVerse account	You will need a CyVerse account to complete this exercise	Register

2.2 Platform(s)

We will use the following CyVerse platform(s):

Platform	Interface	Link	Platform Documenta- tion	Learning Center Docs
Discovery Environ- ment	Web/Point-and- click	Discovery Environ- ment	DE Manual	Guide

2.3 Input and example data

In order to complete this quickstart you will need to have the following inputs prepared

Input File(s)	Format	Preparation/Notes	Example Data
Sequencing reads	FastQ	Any sequencing reads in FastQ format will work. They do not need to be pre-processed. They may also be compressed (e.g. fastq.gz)	gut microbiome (iplantcollaborative > example_data > qiime2 and select gut-microbiome folder)

Get started: Launch JupyterLab-QIIME2

1. Login to the .
2. Click on **Apps** window in the DE workspace and search for and run JupyterLab-Qiime2-2018.11.
3. Under “Analysis Name” leave the defaults or make any desired notes.
4. Under “Parameters” for ‘Input folder’ or ‘Input files’, click Browse, then navigate to and select one or more FastQ files to analyze; Then click OK.

Note: To use our example data, navigate to *Community Data > iplantcollaborative > example_data > qiime2* and select *gut-microbiome* folder.

5. Click **Launch Analysis**. You will receive a notification that the job has been submitted and running with the “Access your running analysis here”.
6. Clicking on the “Access your running analysis” will open the JupyterLab-QIIME2 in another tab in the browser after a brief building phase.

Note: You will be asked to authenticate again to the JupyterLab with your CyVerse username and password

7. You will see the input data under “vice” folder of the JupyterLab. Now you can upload your own Jupyter Notebook or create one using one of the available kernels

Warning: Do not create or store any outputs inside the input folder (gut-microbiome) as those outputs are not brought back after the analysis

8. Finally, once you finish analysis, navigate to the DE tab, select the Analysis window and select the analysis, click “save and complete analysis”. Upon clicking complete analysis, the analysis will be completed and all the outputs will be brought back to the analysis folder.
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3.1 Additional information, help

- Full materials for the webinar is available [here](#)
 - See the original [JupyterLab quick start](#)
 - See the original [qiime2.org](#) for how to run qiime2 analysis
 - Search for an answer: [CyVerse Learning Center](#) or [CyVerse Wiki](#)
 - Contact CyVerse support by clicking the intercom button on the page.
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Fix or improve this documentation

- On Github: [Repo link](#)
 - Send feedback: Tutorials@CyVerse.org
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